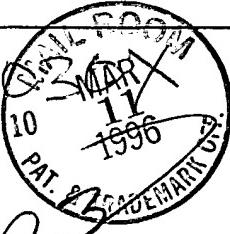


SEQUENCE LISTING



(1) GENERAL INFORMATION:

(i) APPLICANT: NOONBERG, SARAH B.  
HUNT, C. ANTHONY

(ii) TITLE OF INVENTION: IN VIVO OLIGONUCLEOTIDE GENERATOR, AND  
METHODS OF TESTING THE BINDING AFFINITY OF TRIPLEX FORMING  
OLIGONUCLEOTIDES DERIVED THEREFROM

(iii) NUMBER OF SEQUENCES: 25

(iv) CORRESPONDENCE ADDRESS:

- (A) ADDRESSEE: MORRISON & FOERSTER
- (B) STREET: 755 PAGE MILL ROAD
- (C) CITY: PALO ALTO
- (D) STATE: CA
- (E) COUNTRY: USA
- (F) ZIP: 94304-1018

(v) COMPUTER READABLE FORM:

- (A) MEDIUM TYPE: Floppy disk
- (B) COMPUTER: IBM PC compatible
- (C) OPERATING SYSTEM: PC-DOS/MS-DOS
- (D) SOFTWARE: PatentIn Release #1.0, Version #1.30

(vi) CURRENT APPLICATION DATA:

- (A) APPLICATION NUMBER: US 08/324,001
- (B) FILING DATE: 13-OCT-1994
- (C) CLASSIFICATION:

(viii) ATTORNEY/AGENT INFORMATION:

- (A) NAME: MONROY, GLADYS H.
- (B) REGISTRATION NUMBER: 32,430
- (C) REFERENCE/DOCKET NUMBER: 22000-20544.20

(ix) TELECOMMUNICATION INFORMATION:

- (A) TELEPHONE: (415) 813-5600
- (B) TELEFAX: (415) 494-0792
- (C) TELEX: 706141 MRSN FOERSSFO

(2) INFORMATION FOR SEQ ID NO:1:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 38 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

TCGACTCCTC TTCCCTCCTCC ACCTCCTCCT CCCATGCA

(2) INFORMATION FOR SEQ ID NO:2:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 38 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

TCGACCTCCC TTCCCTTCCC TTCCCCTTCC TCCATGCA

38

*A3*  
*Cent*  
(2) INFORMATION FOR SEQ ID NO:3:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 40 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:

TCGACATGAG CATTCACTAG GCGGGCAAGA ATGTGATGCA

40

(2) INFORMATION FOR SEQ ID NO:4:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 39 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:

TCGAGCATGG CCCCTGCGCA AGGATGACAC GCAAATGCA

39

(2) INFORMATION FOR SEQ ID NO:5:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 38 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5:

TCGACCGCCC CGCCCTGCCA CTCATCGCAG TACATGCA

38

(2) INFORMATION FOR SEQ ID NO:6:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 40 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:6:

TCGACTTTTC TCCATTTAG CTTCCTTAGC TCCTGATGCA

40

*13*  
Cert  
(2) INFORMATION FOR SEQ ID NO:7:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 21 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:7:

GTCCTAGGCT TTTGCACTTT T

21

(2) INFORMATION FOR SEQ ID NO:8:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 21 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:8:

GTCCTAGGCT TTTGCACTTT T

21

(2) INFORMATION FOR SEQ ID NO:9:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 21 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

(iv) ANTI-SENSE: YES

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:9:

AAAAGTCCAA AAGCCTAGGA C

21

(2) INFORMATION FOR SEQ ID NO:10:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 50 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:10:

ATTCTTATAC TTCCCTCAAGC AGCCCTCCTC CTCCACCTCC TCCTTCTCCT

50

*103*  
*cont*  
(2) INFORMATION FOR SEQ ID NO:11:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 50 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:11:

AGGAGAAAGGA GGAGGTGGAG GAGGAGGGCT GCTTGAGGAA GTATAAGAAT

50

(2) INFORMATION FOR SEQ ID NO:12:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 28 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:12:

UCCUCUUCCU CCUCCCCCUC CUCCUCCC

28

(2) INFORMATION FOR SEQ ID NO:13:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 28 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:13:

GGGAGGAGGA GGGGGAGGAG GAAGAGGA

28

(2) INFORMATION FOR SEQ ID NO:14:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 82 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: both

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:14:

GUGCUCGCCUU CGGCAGCACUAUCCUCGAC CUCCCCUCCC UUCCCCUJCCC CUUCCUCCAU 60  
GCAUGAAGCG UUCCAUUUUU 82

*A 3/*  
*Cont*  
(2) INFORMATION FOR SEQ ID NO:15:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 84 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: both

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:15:

GUGCUCGCCUU CGGCAGCACUAUCCUCGAC AUGAGCAUUC AUCAGGCAGGG CAAGAAUGUG 60  
AUGCAUGAAG CGUUCCAUUUUU 84

(2) INFORMATION FOR SEQ ID NO:16:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 28 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:16:

UCCUCUUCCCU CCUCCCCCUC CUCCUCCC 28

(2) INFORMATION FOR SEQ ID NO:17:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 58 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:17:

CCCAATCACAGGAGGAG GAGGTGGAGG AGGAGGGCTG CTTGAGGAAG TATAAGAA 58

(2) INFORMATION FOR SEQ ID NO:18:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 58 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

(iv) ANTI-SENSE: YES

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:18:

TTCTTATACT TCCTCAAGCA GCCCTCCTCC TCCACCTCCT CCTTCTCCTG TGATTGGG

58

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Cont

(2) INFORMATION FOR SEQ ID NO:19:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 43 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:19:

CAAGCAGCCC TCCTCCTCCA CCTCCTCCTT CTCCTGTGAT TGG

43

(2) INFORMATION FOR SEQ ID NO:20:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 43 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:20:

CCAATCACAG GAGAAGGAGG AGGTGGAGGA GGAGGGCTGC TTG

43

(2) INFORMATION FOR SEQ ID NO:21:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 28 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:21:

UCCUCUUCCU CCUCCCCCUC CUCCUCCC

28

(2) INFORMATION FOR SEQ ID NO:22:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 28 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:22:

GGGAGGAGGA GGGGGAGGAG GAAGAGGA

28

(2) INFORMATION FOR SEQ ID NO:23:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 28 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:23:

GGGCCCCCCC UCGAGGUCGA CGGUAUUCG

28

(2) INFORMATION FOR SEQ ID NO:24:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 323 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:24:

TTCCCATGAT TCCTTCATAT TTGCATATAC GATACAAGGC TGTTAGAGAG ATAATTAGAA 60  
TTAATTTGAC TGTAAACACA AAGATATTAG TACAAAATAC GTGACGTAGA AAGTAATAAT 120  
TTCTTGGGTA GTTGCAGTT TTTAAAATTA TGTTTTAAAA TGGACTATCA TATGCTTACC 180  
GTAACTTGAA AGTATTTCGA TTTCTTGGCT TTATATATCT TGTGGAAAGG ACGAACACC 240  
GTGCTCGCTT CGGCAGCACA TATCCTCGAG CATGGCCCCT GCGCAAGGAT GACACGCAA 300  
TGCATGAAGC GTTCCATATT TTT 323

(2) INFORMATION FOR SEQ ID NO:25:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 322 base pairs  
(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:25:

TTCCCATGAT TCCTTCATAT TTGCATATAAC GATACAAGGC TGTTAGAGAG ATAATTAGAA 60  
TTAATTTGAC TGTAAACACA AAGATATTAG TACAAAATAC GTGACGTAGA AAGTAATAAT 120  
TTCTTGGGTA GTTGCGAGTT TTTAAAATTA TGTTTTAAAA TGGACTATCA TATGCTTACC 180  
GTAACTTGAA AGTATTCGA TTTCTTGGCT TTATATATCT TGTGGAAAGG ACGAAACACC 240  
GTGCTCGCTT CGGCAGCACA TATCCTCGAC TCCTCTTCCT CCTCCACCTC CTCCTCCCAT 300  
GCATGAAGCG TTCCATATTT TT 322

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cont.